

Rec'd PCT/PTO 21 SEP 2004



10/507275

PCT

RAW SEQUENCE LISTING

DATE: 09/21/2004

PATENT APPLICATION: US/10/507,275

TIME: 09:32:34

Input Set : A:\82368-11.app

Output Set: N:\CRF4\09212004\J507275.raw

3 <110> APPLICANT: Masai, Hisao
 4 Tamai, Katsuyuki
 5 Medical and Biological Laboratories Co., Ltd.
 6 Japan Science and Technology Agency
 7 Ginkgo Biomedical Research Institute Co., Ltd.
 9 <120> TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
 10 Specific Antibodies to the Substrates, and Screening Methods
 11 Using the Same to Screen for Compounds Comprising Cdc7-ASK
 12 Kinase Inhibitory Ability
 14 <130> FILE REFERENCE: 082368-001100US
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/507,275
 C--> 17 <141> CURRENT FILING DATE: 2004-09-09
 19 <150> PRIOR APPLICATION NUMBER: JP 2002-067702
 20 <151> PRIOR FILING DATE: 2002-03-12
 22 <150> PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
 23 <151> PRIOR FILING DATE: 2003-03-12
 25 <160> NUMBER OF SEQ ID NOS: 21
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 130
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Homo sapiens
 34 <400> SEQUENCE: 1
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 36 1 5 10 15
 38 Ser Ser Pro Gly Arg Ser Ser Arg Arg Thr Asp Ala Leu Thr Ser Ser
 39 20 25 30
 41 Pro Gly Arg Asp Leu Pro Pro Phe Glu Asp Glu Ser Glu Gly Leu Leu
 42 35 40 45
 44 Gly Thr Glu Gly Pro Leu Glu Glu Glu Glu Asp Gly Glu Glu Leu Ile
 45 50 55 60
 47 Gly Asp Gly Met Glu Arg Asp Tyr Arg Ala Ile Pro Glu Leu Asp Ala
 48 65 70 75 80
 50 Tyr Glu Ala Glu Gly Leu Ala Leu Asp Asp Glu Asp Val Glu Glu Leu
 51 85 90 95
 53 Thr Ala Ser Gln Arg Glu Ala Ala Glu Arg Ala Met Arg Gln Arg Asp
 54 100 105 110
 56 Arg Glu Ala Gly Arg Gly Leu Gly Arg Met Arg Arg Gly Leu Leu Tyr
 57 115 120 125
 59 Asp Ser
 60 130
 63 <210> SEQ ID NO: 2
 64 <211> LENGTH: 3379



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70 <222> LOCATION: (31)..(2709)
72 <400> SEQUENCE: 2
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75                               1           5
77 cgg cga ggc aat gat cct ctc acc tcc agc cct ggc cga agc tcc cgg 102
78 Arg Arg Gly Asn Asp Pro Leu Thr Ser Ser Pro Gly Arg Ser Ser Arg
79   10           15           20
81 cgt act gat gcc ctc acc tcc agc cct ggc cgt gac ctt cca cca ttt 150
82 Arg Thr Asp Ala Leu Thr Ser Ser Pro Gly Arg Asp Leu Pro Pro Phe
83  25           30           35           40
85 gag gat gag tcc gag ggg ctc cta ggc aca gag ggg ccc ctg gag gaa 198
86 Glu Asp Glu Ser Glu Gly Leu Leu Gly Thr Glu Gly Pro Leu Glu Glu
87           45           50           55
89 gaa gag gat gga gag gag ctc att gga gat ggc atg gaa agg gac tac 246
90 Glu Glu Asp Gly Glu Glu Leu Ile Gly Asp Gly Met Glu Arg Asp Tyr
91           60           65           70
93 cgc gcc atc cca gag ctg gac gcc tat gag gcc gag gga ctg gct ctg 294
94 Arg Ala Ile Pro Glu Leu Asp Ala Tyr Glu Ala Glu Gly Leu Ala Leu
95           75           80           85
97 gat gat gag gac gta gag gag ctg acg gcc agt cga agg gag gca gca 342
98 Asp Asp Glu Asp Val Glu Glu Leu Thr Ala Ser Arg Arg Glu Ala Ala
99   90           95           100
101 gac ggg cca tgc ggc acg gtg acc ggg agc tgg ccg ggg ctg ggc gca 390
102 Asp Gly Pro Cys Gly Thr Val Thr Gly Ser Trp Pro Gly Leu Gly Ala
103 105           110           115           120
105 tgc gcc gtg ggc tcc tgt atg aca gcg atg agg agg acg agg agc gcc 438
106 Cys Ala Val Gly Ser Cys Met Thr Ala Met Arg Arg Thr Arg Ser Ala
107           125           130           135
109 ctg ccc gca agc gcc gcc agt gga gcc ggc acg gag gac ggc gag gag 486
110 Leu Pro Ala Ser Ala Ala Ser Gly Ala Gly Thr Glu Asp Gly Glu Glu
111           140           145           150
113 gac gag cag atg att gag agc atc gag aac ctg gag gat ctc aaa ggc 534
114 Asp Glu Gln Met Ile Glu Ser Ile Glu Asn Leu Glu Asp Leu Lys Gly
115           155           160           165
117 cac tct gtg cgc gag tgg gtg agc atg gcg ggc ccc ccg ctg gag atc 582
118 His Ser Val Arg Glu Trp Val Ser Met Ala Gly Pro Arg Leu Glu Ile
119           170           175           180
121 cac cac cgc ttc aag aac ttc ctg cgc act cac gtc gac agc cac ggc 630
122 His His Arg Phe Lys Asn Phe Leu Arg Thr His Val Asp Ser His Gly
123 185           190           195           200
125 cac aac gtc ttc aag gag cgc atc agc gac atg tgc aaa gag aac cgt 678
126 His Asn Val Phe Lys Glu Arg Ile Ser Asp Met Cys Lys Glu Asn Arg
127           205           210           215
129 gag agc ctg gtg gtg aac tat gag gac ttg gca gcc agg gag cac gtg 726

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130	Glu	Ser	Leu	Val	Val	Asn	Tyr	Glu	Asp	Leu	Ala	Ala	Arg	Glu	His	Val	
131				220					225					230			
133	ctg	gcc	tac	ttc	ctg	cct	gag	gca	ccg	gcg	gag	ctg	ctg	cag	atc	ttt	.774
134	Leu	Ala	Tyr	Phe	Leu	Pro	Glu	Ala	Pro	Ala	Glu	Leu	Leu	Gln	Ile	Phe	
135			235					240					245				
137	gat	gag	gct	gcc	ctg	gag	gtg	gta	ctg	gcc	atg	tac	ccc	aag	tac	gac	822
138	Asp	Glu	Ala	Ala	Leu	Glu	Val	Val	Leu	Ala	Met	Tyr	Pro	Lys	Tyr	Asp	
139		250					255				260						
141	cgc	atc	acc	aac	cac	atc	cat	gtc	cgc	atc	tcc	cac	ctg	cct	ctg	gtg	870
142	Arg	Ile	Thr	Asn	His	Ile	His	Val	Arg	Ile	Ser	His	Leu	Pro	Leu	Val	
143	265					270				275					280		
145	gag	gag	ctg	cgc	tgc	ctg	agg	cag	ctg	cat	ctg	aac	cag	ctg	atc	cgc	918
146	Glu	Glu	Leu	Arg	Ser	Leu	Arg	Gln	Leu	His	Leu	Asn	Gln	Leu	Ile	Arg	
147				285					290				295				
149	acc	agt	ggg	gtg	gtg	acc	agc	tgc	act	ggc	gtc	ctg	ccc	cag	ctc	agc	966
150	Thr	Ser	Gly	Val	Val	Thr	Ser	Cys	Thr	Gly	Val	Leu	Pro	Gln	Leu	Ser	
151			300					305					310				
153	atg	gtc	aag	tac	aac	tgc	aac	aag	tgc	aat	ttc	gtc	ctg	ggt	cct	ttc	1014
154	Met	Val	Lys	Tyr	Asn	Cys	Asn	Lys	Cys	Asn	Phe	Val	Leu	Gly	Pro	Phe	
155			315				320				325						
157	tgc	cag	tcc	cag	aac	cag	gag	gtg	aaa	cca	ggc	tcc	tgt	cct	gag	tgc	1062
158	Cys	Gln	Ser	Gln	Asn	Gln	Glu	Val	Lys	Pro	Gly	Ser	Cys	Pro	Glu	Cys	
159		330				335				340							
161	cag	tgc	gcc	ggc	ccc	ttt	gag	gtc	aac	atg	gag	gag	acc	atc	tat	cag	1110
162	Gln	Ser	Ala	Gly	Pro	Phe	Glu	Val	Asn	Met	Glu	Glu	Thr	Ile	Tyr	Gln	
163	345					350				355					360		
165	aac	tac	cag	cgt	atc	cga	atc	cag	gag	agt	cca	ggc	aaa	gtg	gcg	gct	1158
166	Asn	Tyr	Gln	Arg	Ile	Arg	Ile	Gln	Glu	Ser	Pro	Gly	Lys	Val	Ala	Ala	
167				365					370				375				
169	cgg	cgg	ctg	ccc	cgc	tcc	aag	gac	gcc	att	ctc	ctc	gca	gat	ctg	gtg	1206
170	Arg	Arg	Leu	Pro	Arg	Ser	Lys	Asp	Ala	Ile	Leu	Leu	Ala	Asp	Leu	Val	
171			380					385					390				
173	gac	agc	tgc	aac	gca	gga	gac	gag	ata	gag	ctg	act	ggc	atc	tat	cac	1254
174	Asp	Ser	Cys	Asn	Ala	Gly	Asp	Glu	Ile	Glu	Leu	Thr	Gly	Ile	Tyr	His	
175			395				400				405						
177	aac	aac	tat	gat	ggc	tcc	ctc	aac	act	gcc	aat	ggc	ttc	cct	gtc	ttt	1302
178	Asn	Asn	Tyr	Asp	Gly	Ser	Leu	Asn	Thr	Ala	Asn	Gly	Phe	Pro	Val	Phe	
179		410				415				420							
181	gcc	act	gtc	atc	cta	gcc	aac	cac	gtg	gcc	aag	aag	gac	aac	aag	gtt	1350
182	Ala	Thr	Val	Ile	Leu	Ala	Asn	His	Val	Ala	Lys	Lys	Asp	Asn	Lys	Val	
183	425					430				435					440		
185	gct	gta	ggg	gaa	ctg	acc	gat	gaa	gat	gtg	aag	atg	atc	act	agc	ctc	1398
186	Ala	Val	Gly	Glu	Leu	Thr	Asp	Glu	Asp	Val	Lys	Met	Ile	Thr	Ser	Leu	
187				445				450					455				
189	tcc	aag	gat	cag	cag	atc	gga	gag	aag	atc	ttt	gcc	agc	att	gct	cct	1446
190	Ser	Lys	Asp	Gln	Gln	Ile	Gly	Glu	Lys	Ile	Phe	Ala	Ser	Ile	Ala	Pro	
191			460					465					470				
193	tcc	atc	tat	ggt	cat	gaa	gac	atc	aag	aga	ggc	cct	gct	ctg	gcc	ctg	1494
194	Ser	Ile	Tyr	Gly	His	Glu	Asp	Ile	Lys	Arg	Gly	Pro	Ala	Leu	Ala	Leu	

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197 ttc gga ggg gag ccc aaa aac cca ggt ggc aag cac aag gta cgt ggt 1542
198 Phe Gly Gly Glu Pro Lys Asn Pro Gly Gly Lys His Lys Val Arg Gly
199          490          495          500
201 gat atc aac gtg ctc ttg tgc gga gac cct ggc aca gcg aag tcg cag 1590
202 Asp Ile Asn Val Leu Leu Cys Gly Asp Pro Gly Thr Ala Lys Ser Gln
203 505          510          515          520
205 ttt ctc aag tat att gag aaa gtg tcc agc cga gcc atc ttc acc act 1638
206 Phe Leu Lys Tyr Ile Glu Lys Val Ser Ser Arg Ala Ile Phe Thr Thr
207          525          530          535
209 ggc cag ggg gcg tcg gct gtg gcc gtc acg gcg tat gtc cag cgg cac 1686
210 Gly Gln Gly Ala Ser Ala Val Ala Val Thr Ala Tyr Val Gln Arg His
211          540          545          550
213 cct gtc agc agg gag tgg acc ttg gag gct ggg gcc ctg gtt ctg gct 1734
214 Pro Val Ser Arg Glu Trp Thr Leu Glu Ala Gly Ala Leu Val Leu Ala
215          555          560          565
217 gac cga gga gtg tgt ctc att gat gaa ttt gac aag atg aat gac cag 1782
218 Asp Arg Gly Val Cys Leu Ile Asp Glu Phe Asp Lys Met Asn Asp Gln
219          570          575          580
221 gac aga acc agc atc cat gag gcc atg gag caa cag agc atc tcc atc 1830
222 Asp Arg Thr Ser Ile His Glu Ala Met Glu Gln Gln Ser Ile Ser Ile
223 585          590          595          600
225 tcg aag gct ggc atc gtc acc tcc ctg cag gct cgc tgc acg gtc att 1878
226 Ser Lys Ala Gly Ile Val Thr Ser Leu Gln Ala Arg Cys Thr Val Ile
227          605          610          615
229 gct gcc gcc aac ccc ata gga ggg cgc tac gac ccc tcg ctg act ttc 1926
230 Ala Ala Ala Asn Pro Ile Gly Gly Arg Tyr Asp Pro Ser Leu Thr Phe
231          620          625          630
233 tct gag aac gtg gac ctc aca gag ccc atc atc tca cgc ttt gac atc 1974
234 Ser Glu Asn Val Asp Leu Thr Glu Pro Ile Ile Ser Arg Phe Asp Ile
235          635          640          645
237 ctg tgt gtg gtg agg gac acc gtg gac cca gtc cag gac gag atg ctg 2022
238 Leu Cys Val Val Arg Asp Thr Val Asp Pro Val Gln Asp Glu Met Leu
239          650          655          660
241 gcc cgc ttc gtg gtg ggc agc cac gtc aga cac cac ccc agc aac aag 2070
242 Ala Arg Phe Val Val Gly Ser His Val Arg His His Pro Ser Asn Lys
243 665          670          675          680
245 gag gag gag ggg ctg gcc aat ggc agc gct gct gag ccc gcc atg ccc 2118
246 Glu Glu Glu Gly Leu Ala Asn Gly Ser Ala Ala Glu Pro Ala Met Pro
247          685          690          695
249 aac acg tat ggc gtg gag ccc ctg ccc cag gag gtc ctg aag aag tac 2166
250 Asn Thr Tyr Gly Val Glu Pro Leu Pro Gln Glu Val Leu Lys Lys Tyr
251          700          705          710
253 atc atc tac gcc aag gag agg gtc cac ccg aag ctc aac cag atg gac 2214
254 Ile Ile Tyr Ala Lys Glu Arg Val His Pro Lys Leu Asn Gln Met Asp
255          715          720          725
257 cag gac aag gtg gcc aag atg tac agt gac ctg agg aaa gaa tct atg 2262
258 Gln Asp Lys Val Ala Lys Met Tyr Ser Asp Leu Arg Lys Glu Ser Met
259          730          735          740

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261 gcg aca ggc agc atc ccc att acg gtg cgg cac atc gag tcc atg agt 2310
262 Ala Thr Gly Ser Ile Pro Ile Thr Val Arg His Ile Glu Ser Met Ser
263 745 750 755 760
265 cat ggc gga ggc cca cgc gcg cat cca tct gcg gga cta tgt gat cga 2358
266 His Gly Gly Gly Pro Arg Ala His Pro Ser Ala Gly Leu Cys Asp Arg
267 765 770 775
269 aga cga cgt caa cat ggc cat ccg cgt gat gct gga gag ctt cat aga 2406
270 Arg Arg Arg Gln His Gly His Pro Arg Asp Ala Gly Glu Leu His Arg
271 780 785 790
273 cac aca gaa gtt cag cgt cat cgc agc atg cgc aag act ttt gcc cgc 2454
274 His Thr Glu Val Gln Arg His Arg Ser Met Arg Lys Thr Phe Ala Arg
275 795 800 805
277 tac ctt tca ttc cgg cgt gac aac aat gag ctg ttg ctc ttc ata ctg 2502
278 Tyr Leu Ser Phe Arg Arg Asp Asn Asn Glu Leu Leu Leu Phe Ile Leu
279 810 815 820
281 aag cag tta gtg gca gag cag gtg aca tat cag cgc aac cgc ttt ggg 2550
282 Lys Gln Leu Val Ala Glu Gln Val Thr Tyr Gln Arg Asn Arg Phe Gly
283 825 830 835 840
285 gcc cag cag gac act att gag gtc cct gag aag gac ttg gtg gat aag 2598
286 Ala Gln Gln Asp Thr Ile Glu Val Pro Glu Lys Asp Leu Val Asp Lys
287 845 850 855
289 gct cgt cag atc aac atc cac aac ctc tct gca ttt tat gac agt gag 2646
290 Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe Tyr Asp Ser Glu
291 860 865 870
293 ctc ttc agg atg aac aag ttc agc cac gac ctg aaa agg aaa atg atc 2694
294 Leu Phe Arg Met Asn Lys Phe Ser His Asp Leu Lys Arg Lys Met Ile
295 875 880 885
297 ctg cag cag ttc tga ggccctatgc catccataag gattccttgg gattctggtt 2749
298 Leu Gln Gln Phe
299 890
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309 gtgggatgtg agtcatgcgg attatccact cgccacagtt atcagctgcc attgctccct 3289
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311 ataaagttga ataaaatata aaaaaaaaaa 3379
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316 <212> TYPE: PRT
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322 Ser Ser Pro Gly Arg Ser Ser Arg Arg Thr Asp Ala Leu Thr Ser Ser

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date